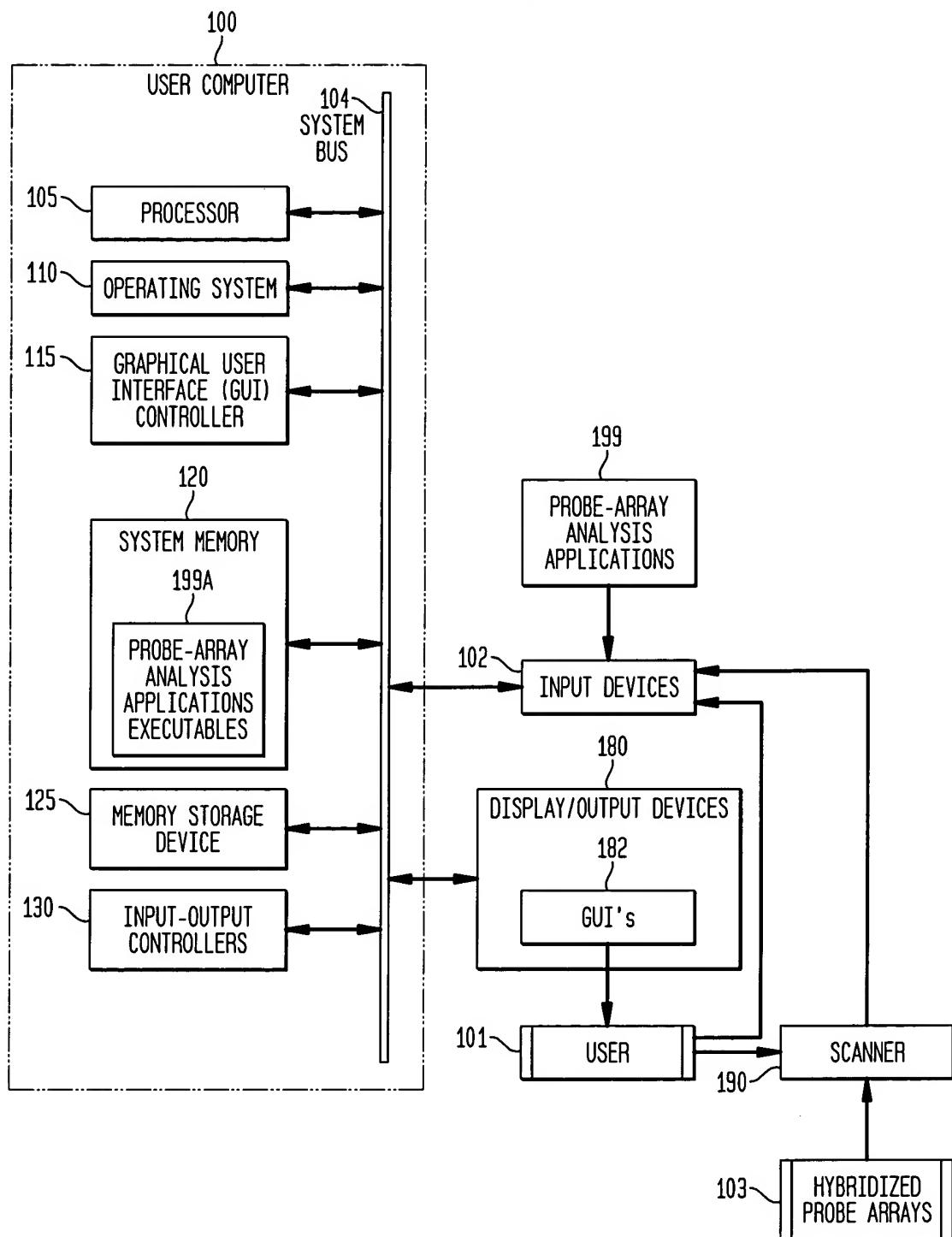


FIG. 1



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FIG. 2

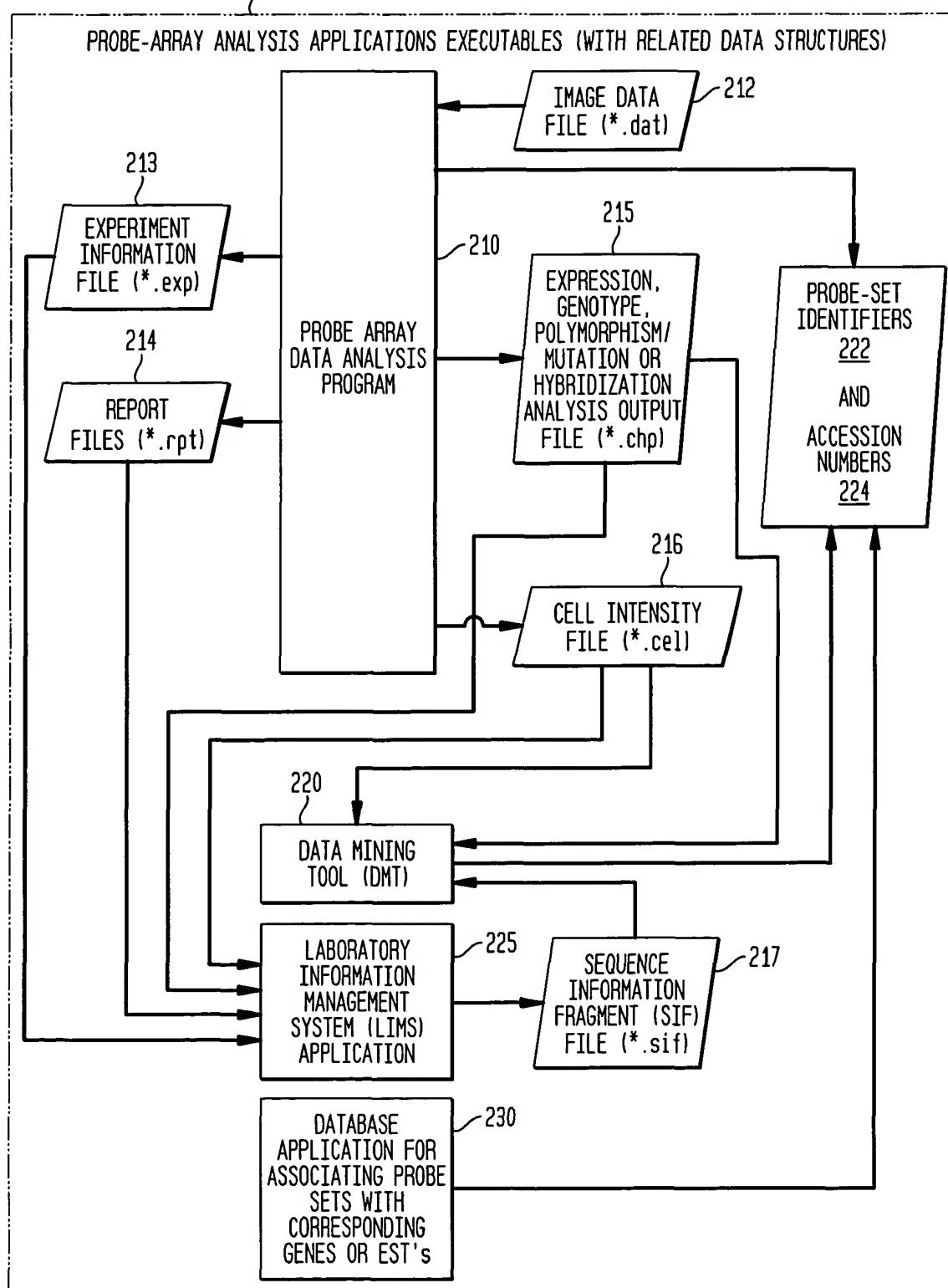


FIG. 3  
(PRIOR ART)

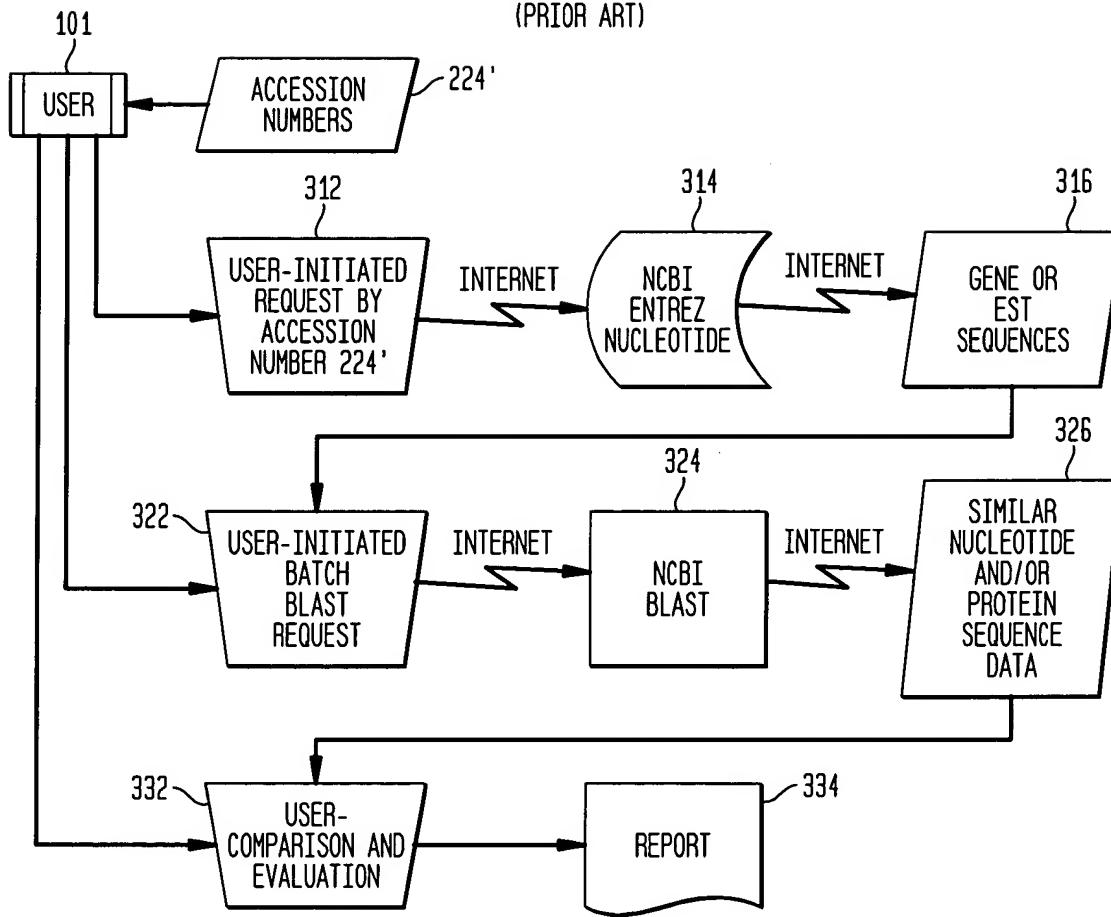
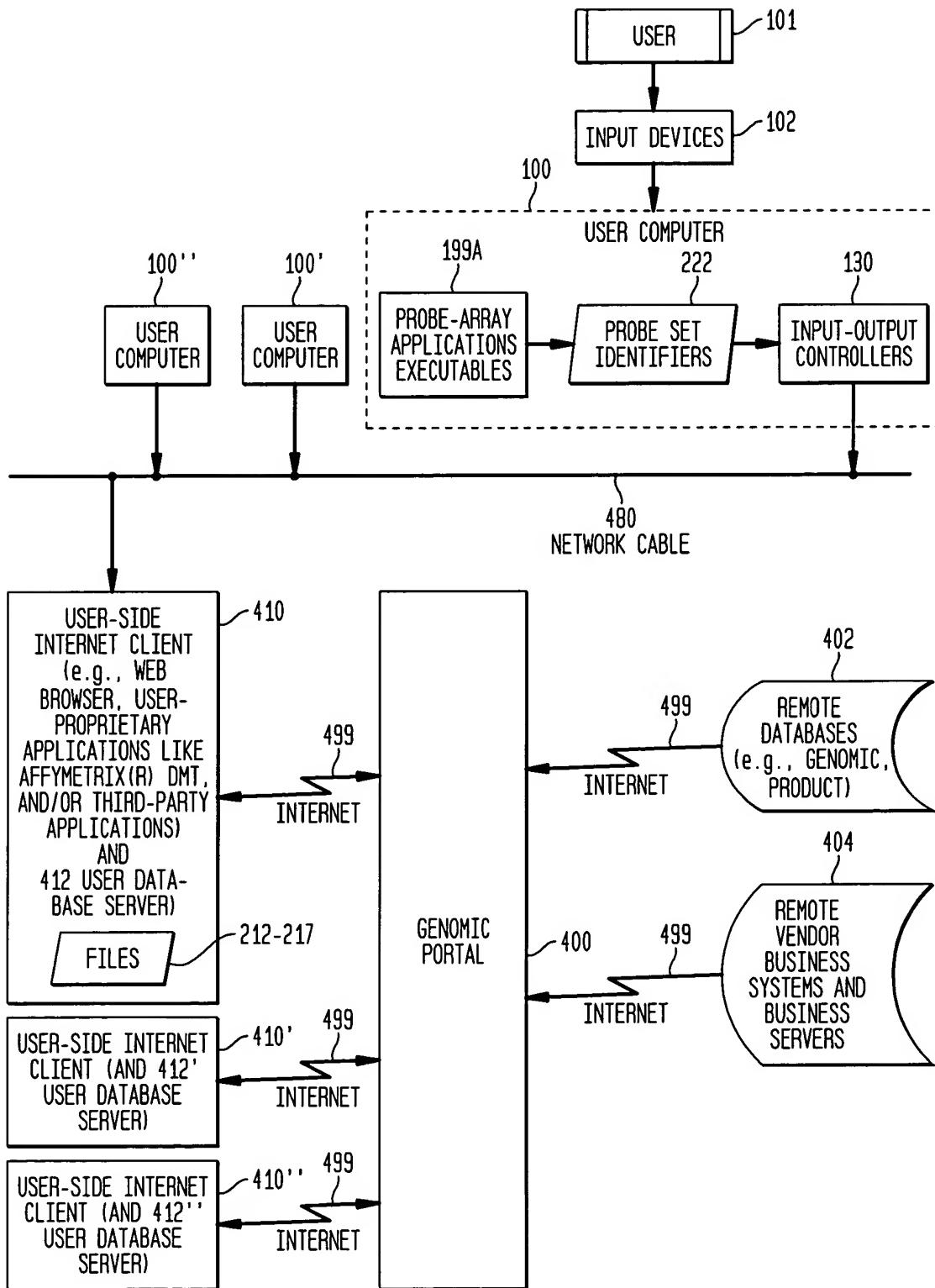




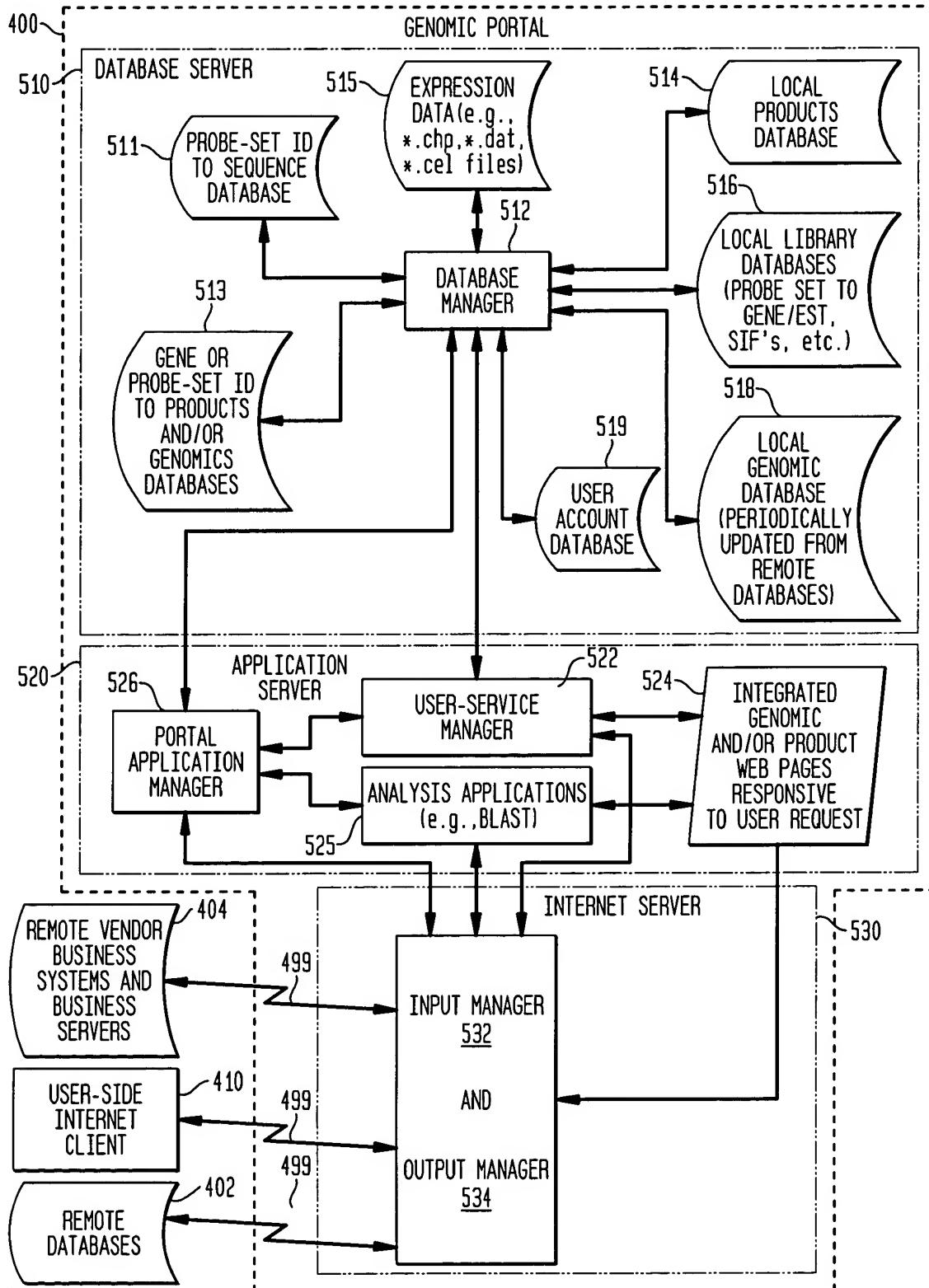
FIG. 4



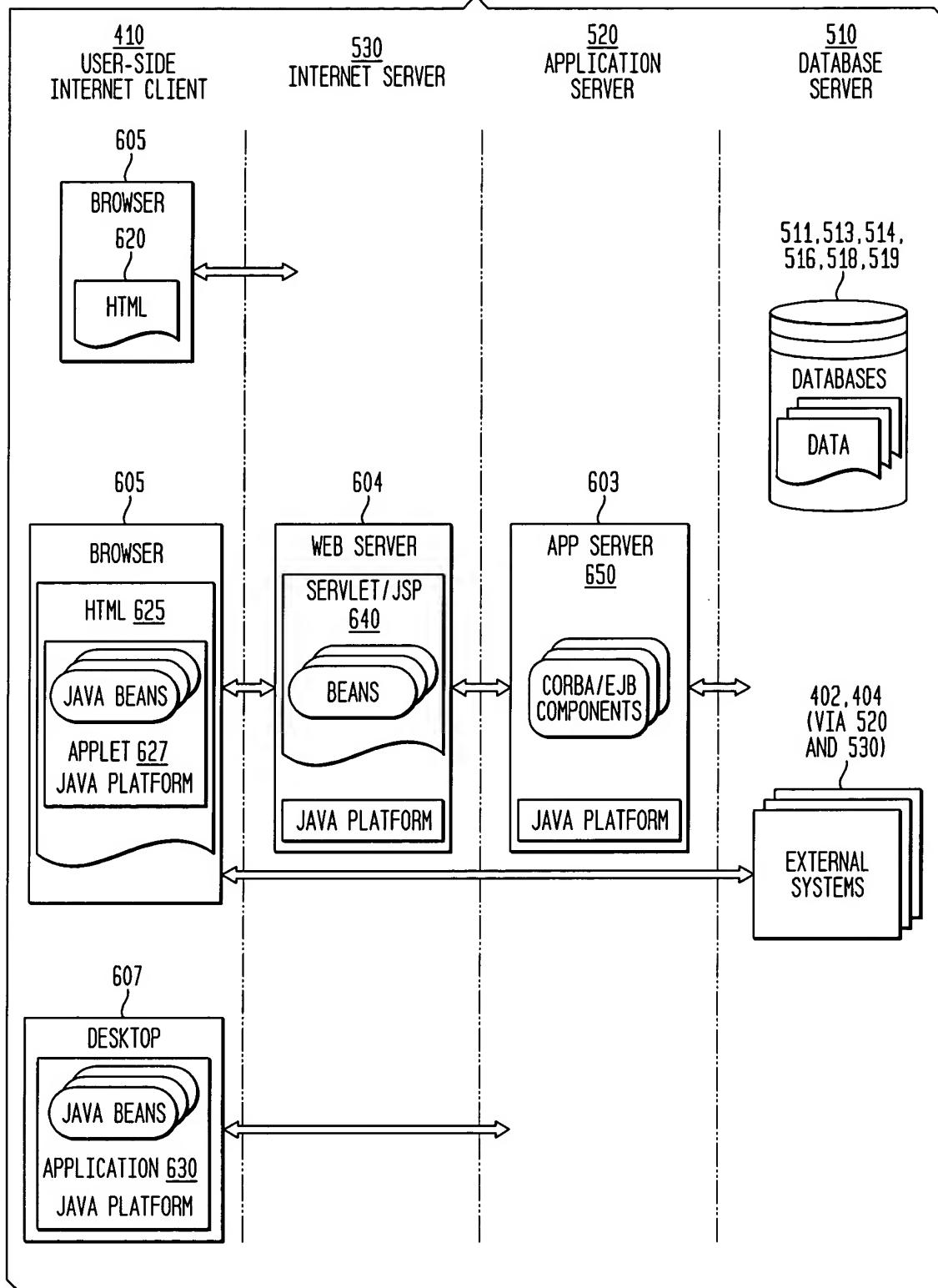


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FIG. 5

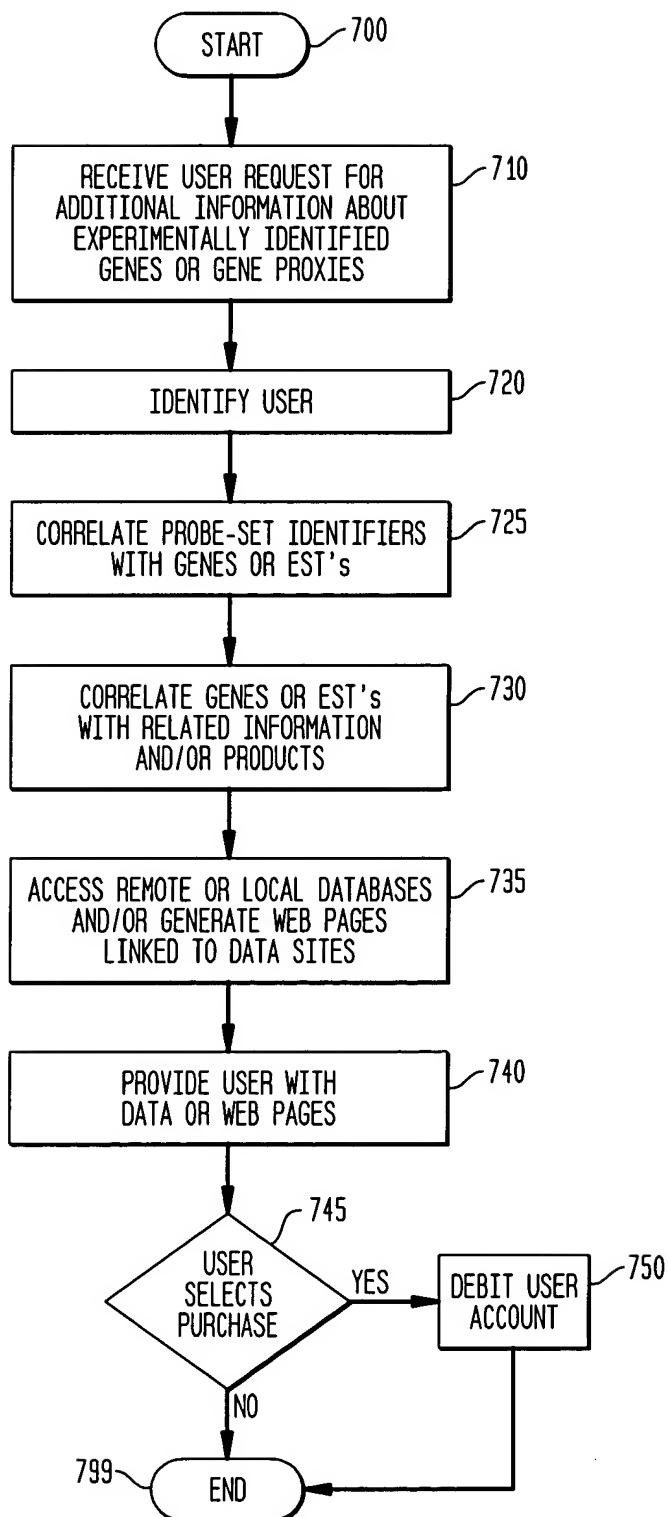


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FIG. 6





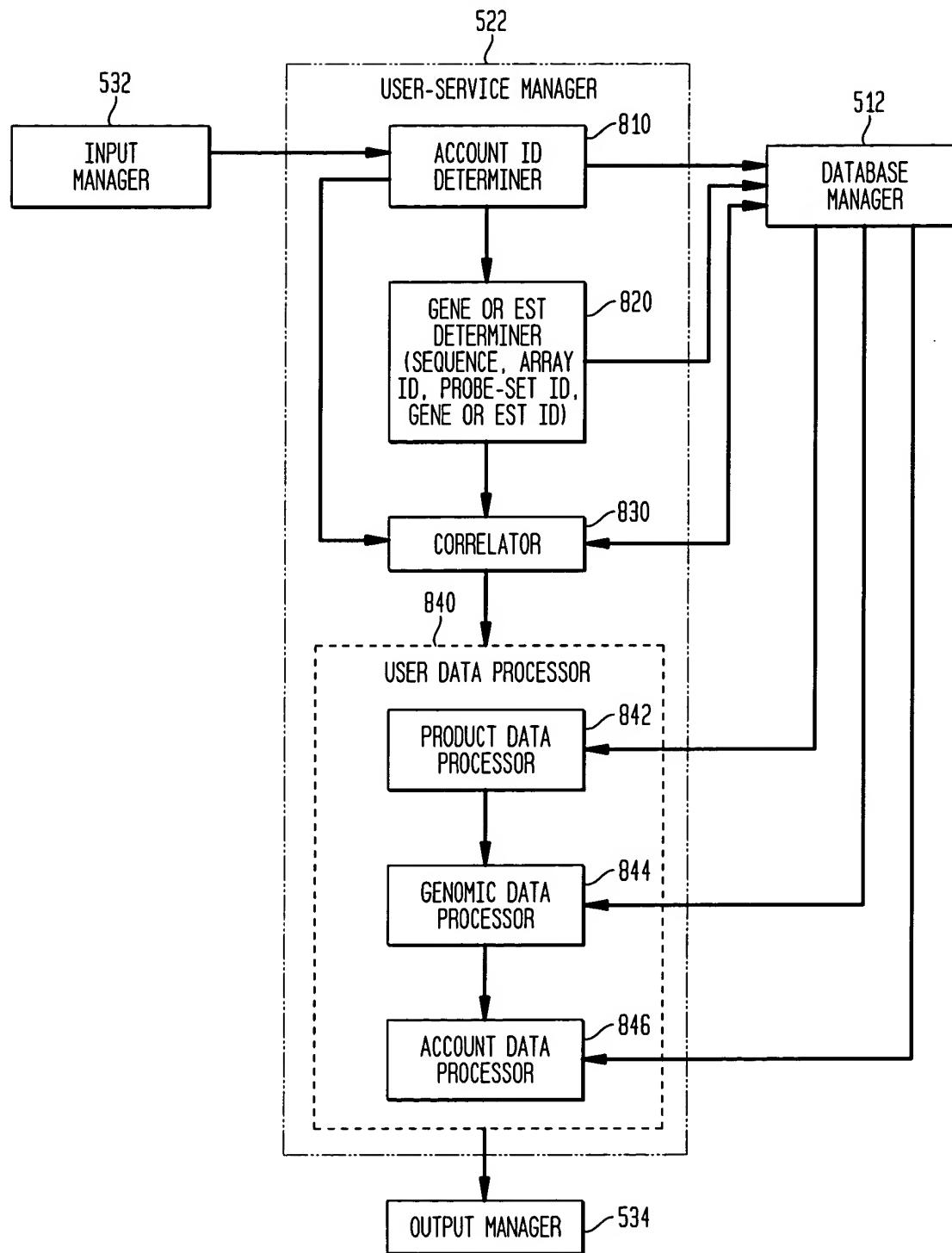
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FIG. 7





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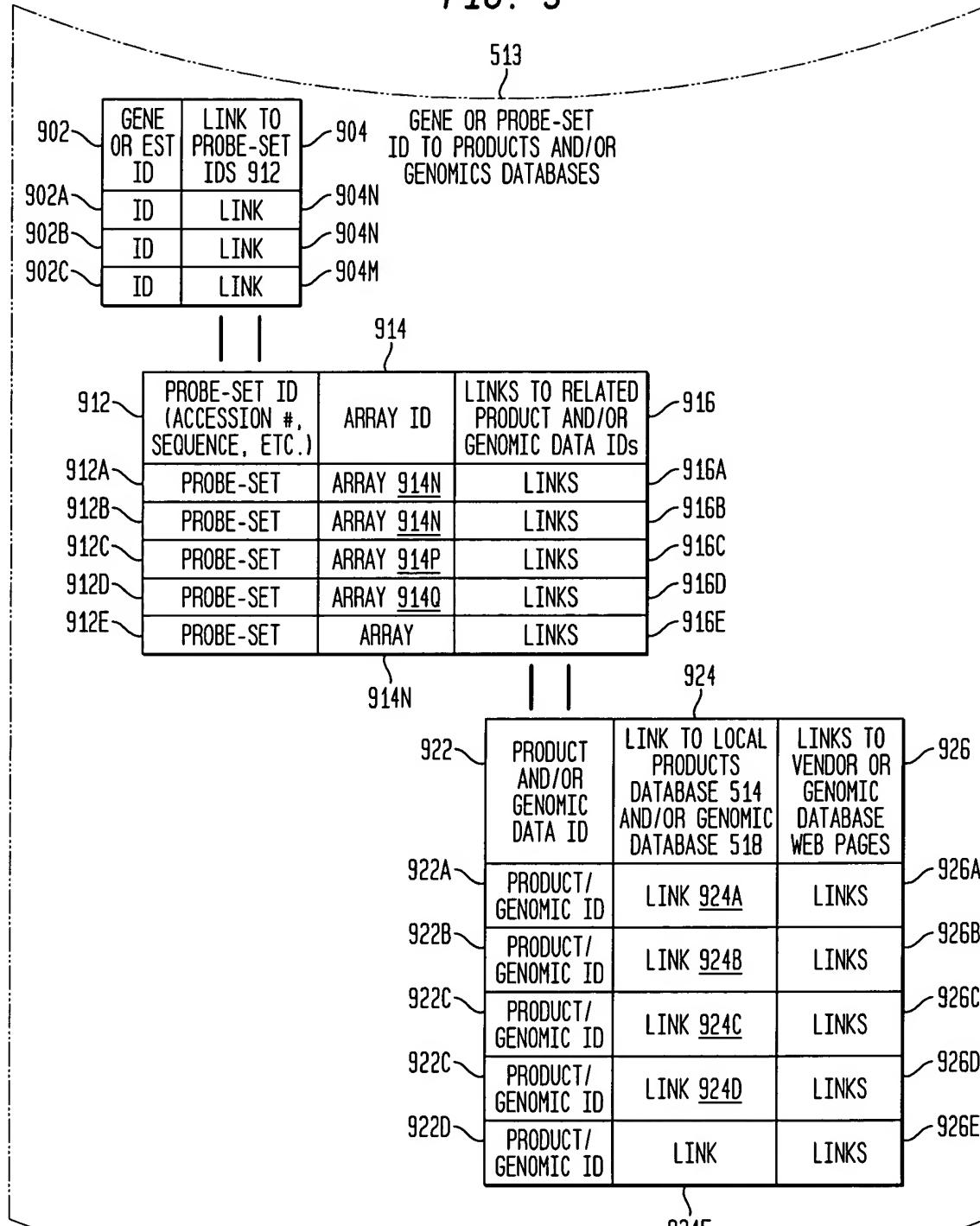
FIG. 8





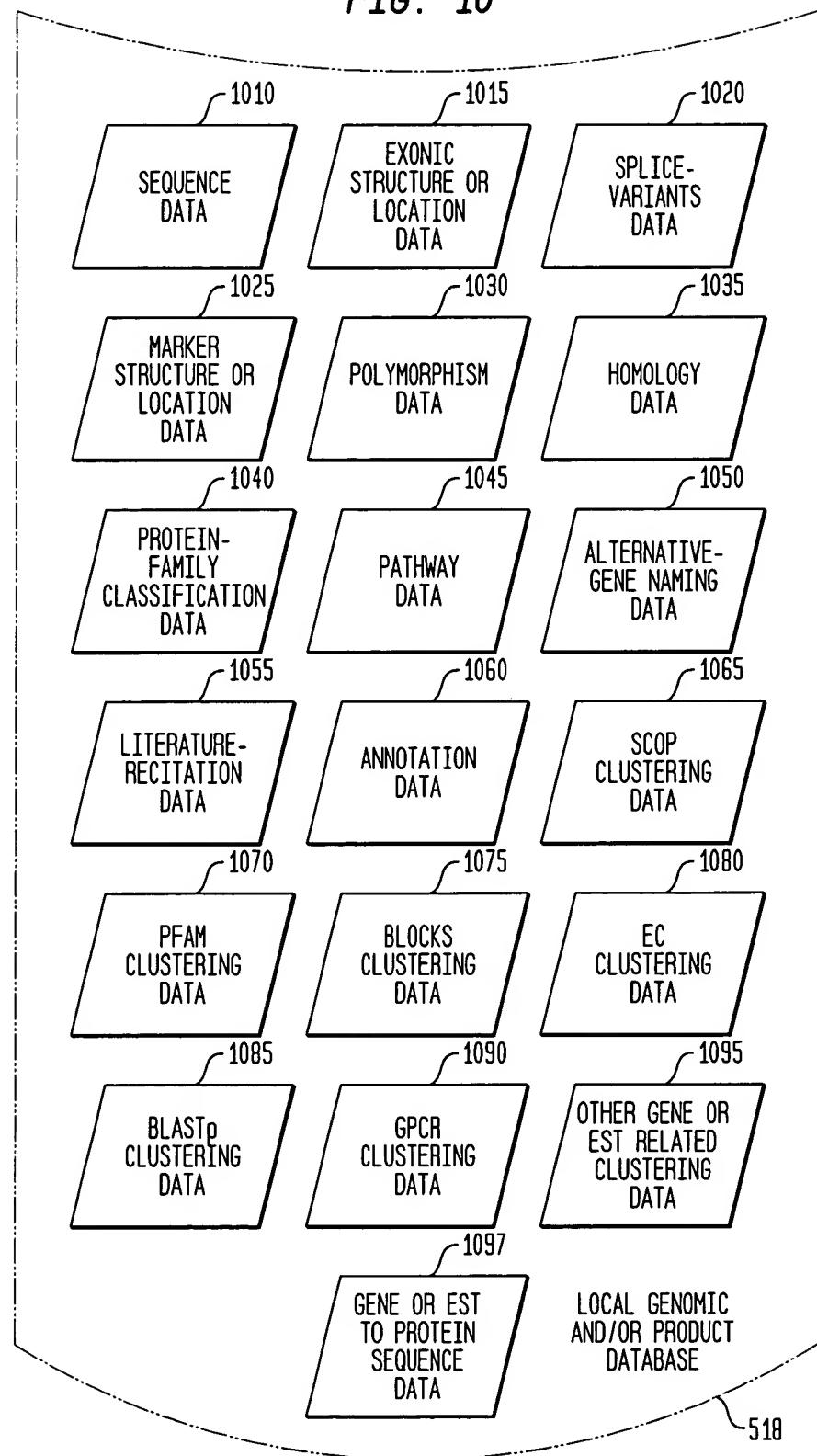
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FIG. 9





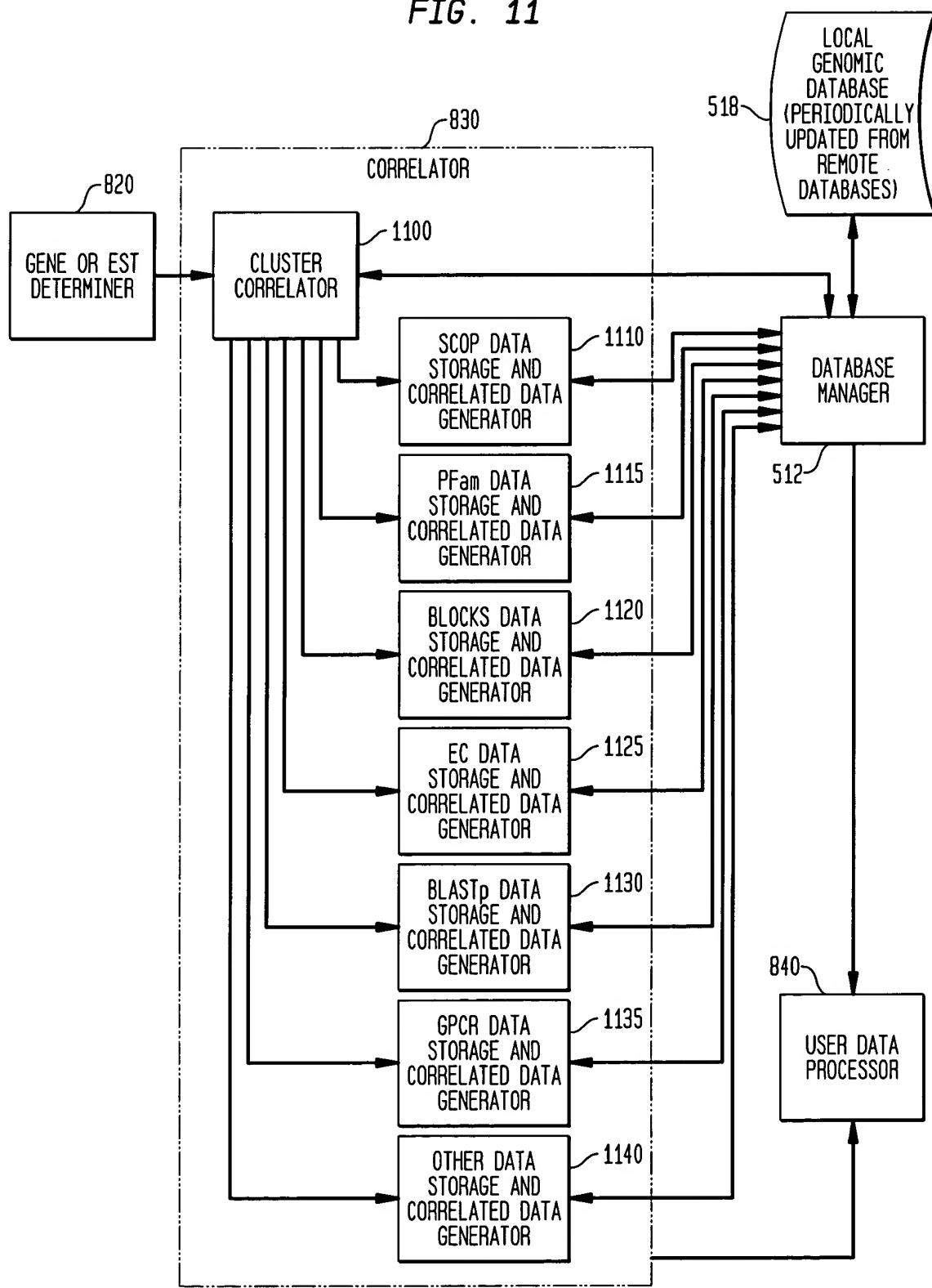
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FIG. 10





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FIG. 11





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FIG. 12

PROTEIN  
IDENTIFIER  
1240

GUI  
1200

Domains\_PFAM\_Hs:NP\_003828

CLUSTER METHOD  
IDENTIFIER  
1210

RETURNED FAMILY  
DATA  
1220

ID NP\_003828

SEARCH\_METHOD hmmpfam

HIT\_NAME FBPase\_WUSTL

HIT\_DESC Fructose-1-6-bisphosphatase

OVERALL\_EXPECT 1.5e-179 LOG10-179

SIMSPAN Query 12 \_ 335 Target 1 \_ 342; EXPECT 1.5e-179 LOG10 -  
179;  
ALIGNMENT

FBPase: domain 1 of 1, from 12 to 335: score 609.9, E = 1.5e-179

\*->iTLtrfileeqgedalaKNEatgeldtlLssLalaakeiartIarag  
+TLtr ++e+ g+ a+ tgelt+ll+s +a k+i+++++ag

NP\_003828 12 LTLTRYVMEK-GRQAK---GTGELTQLLNSMLTAIKAISSAVRKAG  
53

NP\_003828 54 Lan11GlagatNsqGDeQKkLDViaddifinALKasgvavlaSEEedel  
La+1+G+ag++N++GDe+KKLDV+++ ++in+L++S ++v1+SEE++++  
103 LAHLYGIAGSVNVTGDEVKKLDVLSNSLVINMLQSSYSTCVLVSEENKDA

//

1230  
RETURNED ALIGNMENT  
DATA